SEQUENCE LISTING

promiss reprinc
<110> Nemerow, Glen R. Li, Erguang
<120> BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETED GENE DELIVERY
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tca gga cct gag ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc 150 Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys 30 35 40
aag gct tct gga tac aca ttc act gac tac aac atg cac tgg gtg aag 198 Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met His Trp Val Lys 45 50 55
cag agc cat gga aag agc ctt gag tgg att gga tat att tat cct tac 246 Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr 60 65 70
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aca tot gat goo tot goa gto tat tac tgt goa aga ggg att got tac 390 Thr Ser Asp Ala Ser Ala Val Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr 110 115 120

tgg g Trp G	gc ly	caa Gln	999 Gly 125	act Thr	ctg Leu	gtc Val	act Thr	gtc Val 130	tct Ser	gca Ala	gcc Ala	aaa Lys	acg Thr 135	aca Thr	ccc Pro	438
cca t Pro S	er	gtc Val 140	tat Tyr	cca Pro	ctg Leu	gcc Ala	cct Pro 145	gga Gly	tct Ser	gct Ala	gcc Ala	caa Gln 150	act Thr	aac Asn	tcc Ser	486
atg g Met V 1	tg al .55	acc Thr	ctg Leu	gga Gly	tgc Cys	ctg Leu 160	gtc Val	aag Lys	ggc Gly	tat Tyr	ttc Phe 165	cct Pro	gag Glu	cca Pro	gtg Val	534
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cca g Pro A	gct Ala	gtc Val	ctg Leu	cag Gln 190	tct Ser	gac Asp	ctc Leu	tac Tyr	act Thr 195	ctg Leu	agc Ser	agc Ser	tca Ser	gtg Val 200	act Thr	630
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cac c His P	ccg Pro	gcc Ala 220	agc Ser	agc Ser	acc Thr	aag Lys	gtg Val 225	gac Asp	aag Lys	aaa Lys	att Ile	gtg Val 230	ccc Pro	agg Arg	gat Asp	726
tgt g Cys G	ggt Ely 235	tgt Cys	aag Lys	cct Pro	tgc Cys	ata Ile 240	tgt Cys	aca Thr	gtc Val	cca Pro	gaa Glu 245	gta Val	tca Ser	tct Ser	gtc Val	765
ttc a Phe I 250	atc [le	ttc Phe	ccc Pro	cca Pro	aag Lys 255	ccc Pro	aag Lys	gat Asp	gtg Val	ctc Leu 260	acc Thr	att Ile	act Thr	ctg Leu	act Thr 265	822
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acg o	caa Gln	ccc Pro 300	cgg Arg	gag Glu	gag Glu	cag Gln	ttc Phe 305	aac Asn	agc Ser	act Thr	ttc Phe	cgc Arg 310	tca Ser	gtc Val	agt Ser	966
gaa c Glu I	ctt Leu 315	ccc Pro	atc Ile	atg Met	cac His	cag Gln 320	gac Asp	tgg Trp	ctc Leu	aat Asn	ggc Gly 325	aag Lys	gag Glu	ttc Phe	aaa Lys	1014
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cct	ccc	aag	gag	cag	atg	gcc	aag	gat	aaa	gtc	agt	ctg	acc	tgc	atg	1158

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ggg cag cca gcg gag aac tac aag aac act cag ccc atc atg gac aca Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr 395 400 405	1254
gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag agc aac Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn 410 425	1302
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cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt aaa His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys 445 450 455	1395
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Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
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                245
Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
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Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
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Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
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Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
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Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
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                         375
Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
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                                                               400
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Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
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                                      410
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Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
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tgg gtt cca ggc tcc act ggt gac att gtg ctg acc caa tct cca gct
Trp Val Pro Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala
                                                                          99
      15
                                                                         147
 tot ttg got gtg tot ota ggg cag agg god acc atc toc tgc aag god
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala
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 agc caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac caa
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tta gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg aca Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr 80 85 90	291
gac ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca acc Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr 95 100 105	339
tat tac tgt cag caa act aat gag gat ccg tgg acg ttc ggt gga ggc Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro Trp Thr Phe Gly Gly 110 120 125	387
acc aag ctg gaa atc aaa cgg gct gat gct gca cca act gta tcc atc Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile 130 135 140	435
ttc cca cca tcc agt gag cag tta aca tct gga ggt gcc tca gtc gtg Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val 145 150 155	483
tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys 160 165 170	531
att gat ggc agt gaa cga caa aat ggc gtc ctg aac agt tgg act gat Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp 175 180 185	579
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acc aag gac gag tat gaa cga cat aac agc tat acc tgt gag gcc act Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr 210 215 220	675
cac aag aca tca act tca ccc att gtc aag agc ttc aac agg aat gag His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu 225 230 235	723
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Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
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Gln Gln Thr Asn Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
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                             120
Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
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Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
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Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
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Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
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Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
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                                       10
gtc cac tot gag gtc cag ott cag cag toa gga cot gag otg gtg aaa
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Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga tac aca ttc
                                                                         144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                               40
act gac tac aac atg cac tgg gtg aag cag agc cat gga aag agc ctt
Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
                                                                         192
                                                                         240
 gag tgg att gga tat att tat cct tac aaa ggt ggt act ggc tac aac
 Ğlu Trp Ile Gly Tyr Ile Tyr Pro Tyr Lys Gly Gly Thr Gly Tyr Asn
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								ctg Leu 105									336
								tac Tyr									384
								ccc Pro									432
			_	_				tcc Ser	_					_	_		480
								gtg Val									528
								ttc Phe 185									576
			_	_	_			act Thr	-			_	_				624
								gcc Ala									672
								gat Asp									720
								gtc Val									768
								act Thr 265									816
gta Val	gac Asp	atc Ile 275	agc Ser	aag Lys	gat Asp	gat Asp	ccc Pro 280	gag Glu	gtc Val	cag Gln	ttc Phe	agc Ser 285	tgg Trp	ttt Phe	gta Val		864
								cag Gln									912
								agt Ser									960
gac	tgg	ctc	aat	ggc	aag	gag	ttc	aaa	tgc	agg	gtc	aac	agt	gca	gct	1	1008

Asp Trp Leu	Asn Gl 32		Glu	Phe	Lys	Cys 330	Arg	Val	Asn	Ser	Ala 335	Ala	
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aag gct cca Lys Ala Pro 355													1104
aag gat aaa Lys Asp Lys 370													1152
gac att act Asp Ile Thr 385													1200
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Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
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Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
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Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
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Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln
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Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
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Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
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Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
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<211> 157
<212> PRT
<213> Human
<220>
<221> PEPTIDE
<222> (0)...(0)
<223> Tumor necrosis factor-alpha (TNF alpha, mature peptide)
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Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
                85
                                    90
Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
                                105
            100
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
       115
                            120
                                                 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
                        135
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
                    150
<210> 8
<211> 70
<212> PRT
<213> Human
<220>
<221> PEPTIDE
<222> (0) ... (0)
<223> Human Insulin-like Growth Factor 1 sequence
     (IGF-1, mature peptide)
<400> 8
Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
            20
                                25
Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
     35
                          40
                                               45
Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
 50
                        55
Lys Pro Ala Lys Ser Ala
65
<210> 9
<211> 53
<212> PRT
<213> Human
<220>
<221> PEPTIDE
<222> (0)...(0)
<223> Epidermal Growth Factor (EGF, mature peptide)
<400>9
Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
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                5
                                    10
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
                                25
                                                     30
            20
Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
       35
                            40
Trp Trp Glu Leu Arg
   50
<210> 10
<211> 164
<212> PRT
<213> Human
<220>
<221> PEPTIDE
<222> (0)...(0)
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<223> Stem Cell Factor (SCF, mature peptide)
<400> 10
Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr
                                    10
Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr
                                25
           20
                                                    30
Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met
        35
                            40
                                                45
Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser
                        55
Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
                    70
                                        75
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys
                85
                                    90
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro
            100
                                105
Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
        115
                            120
                                                125
Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu
                       135
                                           140
Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu
                    150
Pro Pro Val Ala
<210> 11
<211> 597
<212> PRT
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<213> Artificial Sequence

<223> Fusion protein with N-terminal portion of DAV-1 heavy chain and TNF alpha mature peptide

<400> 11 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly 5 10 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys 20 25 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45 Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu 55 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Lys Gly Gly Thr Gly Tyr Asn 70 75 Gln Lys Phe Lys Ser Lys Ala Thr Leu Thr Thr Asp Ser Ser Ser Asn 85 90 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Asp Ala Ser Ala Val 105 Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr Trp Gly Gln Gly Thr Leu Val 115 120 125 Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala 135 140 Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu 145 150 155 Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly 165 170 175 Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp 185 180 190 Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro 195 200 205

```
Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
                                          220
                        215
    210
Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile
                                        235
                    230
Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
                                                         255
                                    250
                245
Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
                                                     270
                                265
            260
Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val
                                                 285
                            280
        275
Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln
                                             300
                        295
    290
Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
                    310
                                        315
Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
                                                         335
                325
                                    330
Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
                                345
                                                     350
            340
Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
                            360
        355
Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
                        375
    370
Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
                                         395
                    390
Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
                                     410
                405
Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
                                                     430
                                425
Ile Cys Ser Val Leu His Glu Phe Val Arg Ser Ser Ser Arg Thr Pro
                            440
                                                 445
        435
Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
                        455
                                             460
    450
Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
                    470
                                         475
Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
                                                         495
                485
                                     490
Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
                                 505
                                                     510
            500
His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
                            520
                                                 525
        515
Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
                         535
    530
Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
                                         555
                     550
Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
                                     570
                565
Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
                                 585
            580
Gly Ile Ile Ala Leu
        595
<210> 12
<211> 510
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<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein with N-terminal portion of DAV-1 heavy chain and IGF-1 mature peptide

<400> 12

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly

_				_					10					15	
1 Val	His	Ser	Glu 20	5 Val	Gln	Leu	Gln	Gln 25		Gly	Pro	Glu	Leu 30		Lys
Pro	Gly	Ala 35	Ser	Val	Lys	Ile	Ser 40		Lys	Ala	Ser	Gly 45		Thr	Phe
	50	Tyr				55	Val				60				
Glu 65	Trp	Ile	Gly	Tyr	Ile 70	Tyr	Pro	Tyr	Lys	Gly 75	Gly	Thr	Gly	Tyr	Asn 80
Gln				85			Thr		90					95	
			100				Ser	105					TTO		
Tyr	Tyr	Cys 115	Ala	Arg	Gly	Ile	Ala 120	Tyr	Trp	Gly	Gln	Gly 125	Thr	Leu	Val
Thr	Val 130		Ala	Ala	Lys	Thr 135	Thr	Pro	Pro	Ser	Val 140	Tyr	Pro	Leu	Ala
Pro 145	Gly	Ser	Ala	Ala	Gln 150	Thr	Asn	Ser	Met	Val 155	Thr	Leu	Gly	Суѕ	Leu 160
Val	Lys	Gly	Tyr	Phe 165	Pro	Glu	Pro	Val	Thr 170	Val	Thr	Trp	Asn	Ser 175	Gly
Ser	Leu	Ser	Ser 180	Gly	Val	His	Thr	Phe 185	Pro	Ala	Val	Leu	Gln 190	Ser	Asp
Leu	Tyr	Thr 195	Leu	Ser	Ser	Ser	Val 200	Thr	Val	Pro	Ser	Ser 205	Thr	Trp	Pro
Ser	Glu 210	Thr	Val	Thr	Cys	Asn 215	Val	Ala	His	Pro	Ala 220	Ser	Ser	Thr	Lys
225	Asp				230		Arg			235					240
Cys				245	Val		Ser		250					255	
			260	Thr			Leu	265					270		
Val	Asp	Ile 275	Ser	Lys	Asp	Asp	Pro 280	Glu	Val	Gln	Phe	Ser 285	Trp	Phe	Val
_	290	Val	Glu			295	Ala				300				
Phe 305	Asn	Ser	Thr	Phe	Arg 310	Ser	Val	Ser	Glu	Leu 315	Pro	Ile	Met	His	Gln 320
Asp	Trp			325			Phe		330					335	
			340				Thr	345					350		
_		355	,				11e 360					365			
_	370					375	Cys				380				
385	Ile	Thr			390	Gln	. Trp			395					Tyr 400
Lys	Asn			405					410					415	Tyr
	_		420	1				425					430		Phe
Ile	cys	Ser 435		. Lev	His	Glu	Phe 440		Pro	Glu	Thr	Leu 445	. Cys	Gly	Ala
Glu	Leu 450	ı Val	Asp	Ala	Leu	Glr 455		Val	. Сув	Gly	Asp 460	Arg	Gly	Phe	Tyr
Phe 465	a Asr	ı Lys	s Pro	Thr	Gly 470	Tyr		Ser	Ser	Ser 475	Arg	, Arg	, Ala	Pro	Gln 480
Thr	Gl _y	r Ile	e Val	. Asp 485	Glu		Cys	Phe	Arg 490	ser,		a Asp	Leu	Arg 495	Arg
Leu	ı Glu	ı Met	ту1			Pro	Leu	Lys			Lys	Ser	. Ala	L	

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<210> 13
<211> 493
<212> PRT
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<213> Artificial Sequence

<220>

TL

<223> Fusion protein with N-terminal portion of DAV-1 heavy chain and EGF mature peptide

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<400> 13
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
                                25
            20
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                                                45
                            40
Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
   50
                        55
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Lys Gly Gly Thr Gly Tyr Asn
                    70
                                        75
Gln Lys Phe Lys Ser Lys Ala Thr Leu Thr Thr Asp Ser Ser Ser Asn
                85
                                    90
Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Asp Ala Ser Ala Val
                                                    110
                                105
            100
Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr Trp Gly Gln Gly Thr Leu Val
                                                125
                            120
       115
Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala
                                            140
                        135
Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu
                                        155
                    150
Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
                                    170
                165
Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp
                                                     190
            180
                                185
Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro
                                                 205
        195
                            200
Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
                        215
                                            220
Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile
                                        235
                    230
Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
                                                         255
                                    250
                245
Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
                                                     270
                                265
            260
Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val
                                                 285
                            280
        275
Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln
                        295
                                             300
Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
                    310
                                         315
Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
                325
                                     330
Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
                                                    350
            340
                                 345
Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
                                                 365
        355
                            360
Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
                                             380
                         375
Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
385
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```
Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
                            410
               405
Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
                               425
            420
Ile Cys Ser Val Leu His Glu Phe Asn Ser Asp Ser Glu Cys Pro Leu
                                               445
                           440
Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
                                           460
                       455
Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
                                       475
                  470
Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
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<210> 14
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<211> 613

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein with N-terminal portion of DAV-1 heavy chain and SCF mature peptide

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Lys Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Ala Thr Leu Thr Thr Asp Ser Ser Ser Asn Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Asp Ala Ser Ala Val Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln

```
315
                    310
Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
                                 330
            325
Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
                                                    350
                                345
            340
Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
                            360
        355
Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
                                            380
                        375
Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
                                        395
                    390
Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
               405
                                   410
Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
                                425
            420
Ile Cys Ser Val Leu His Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg
                           440
Pro Gln Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val
                        455
Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys
                                       475
                    470
Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu
                                    490
                485
Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe
                                505
            500
Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu
                                                525
                            520
Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
                                            540
                        535
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr
                  550
                                        555
Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys
                                    570
                565
Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr
                                                    590
                                585
            580
Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met
                            600
                                                605
       595
Leu Pro Pro Val Ala
    610
<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence
 <223> PCR primer for amplification of CH3 region of
      DAV-1 heavy chain.
 <400> 15
                                                                        23
 cctgctctgt gtttacatga ggg
 <210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer for amplification of CH1 region of
      DAV-1 heavy chain.
 <400> 16
```

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19
cccagggtca tggagttag
<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence
<223> PCR primer for amplification of DAV-1 kappa chain
      CL-A.
<400> 17
                                                                           20
aagatggata cagttggtgc
<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer for amplification of DAV-1 kappa chain
      CL-B.
<400> 18
                                                                           20
tgtcaagagc ttcaacagga
<210> 19
<211> 15
<212> PRT
<213> Adenovirus
<220>
<221> PEPTIDE
<222> (0)...(0)
<223> Peptide spanning integrin binding site on penton base.
Met Asn Asp His Ala Ile Arg Gly Asp Thr Phe Ala Thr Arg Ala
<210> 20
<211> 9
<212> PRT
<213> Adenovirus
<220>
<221> PEPTIDE
 <222> (0) ... (0)
 <223> Epitope on penton base integrin binding site recognized by DAV-1.
 <400> 20
 Ile Arg Gly Asp Thr Phe Ala Thr Arg
                  5
 <210> 21
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR sense primer for subcloning DAV-1 heavy chain for whole antibody
       or Fab'2 constructs.
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<pre><400> 21 ggtaccgcca ccatgggatg gagctggatc t</pre>	31
<210> 22 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> PCR antisense primer for subcloning DAV-1 heavy chain for whole antibody construct.	
<400> 22 gaattcatgt aacacagagc agga	24
<210> 23 <211> 35 <212> DNA <213> Artificial Sequence	
<220> <223> PCR sense primer for subcloning DAV-1 light chain for whole antibody or Fab'2 constructs.	
<400> 23 aagcttgcca ccatggagac agacacaatc ctgct	35
<210> 24 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> PCR antisense primer for subcloning DAV-1 light chain for whole antibody or Fab'2 constructs.	
<400> 24 tctagatgtc tctaacactc attcctgt	28
<210> 25 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> PCR antisense primer for subcloning DAV-1 heavy chain for Fab'2 constructs.	
<400> 25 gaattetgat aettetggga etgt	24
<210> 26 <211> 26 <212> DNA <213> Artificial Sequence	
<220>	
<400> 26 gaattcgtca gatcatcttc tcgaac	26

<210> 27 <211> 26 <212> DNA <213> Artificial Sequence	
<220>	
<400> 27 gaattctaca gggcaatgat cccaaa	26
<210> 28 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> PCR sense primer for subcloning IGF-1 into DAV-1/IGF-1 fusion construct.	
<400> 28 gaattcggac cggagacget ctgcgg	26
<210> 29 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> PCR antisense primer for subcloning IGF-1 into DAV-1/IGF-1 fusion construct.	
<400> 29 gaattctaag ctgacttggc aggctt	26
<210> 30 <211> 96 <212> DNA <213> Artificial Sequence	
<220> <223> PCR sense primer for subcloning EGF into DAV-1/EGF fusion construct.	
<400> 30 gaattcaata gtgactctga atgtcccctg tcccacgatg ggtactgcct ccatgatggt gtgtgcatgt atattgaagc attggacaag tatgca	60 96
<210> 31 <211> 98 <212> DNA <213> Artificial Sequence	
<220> <223> PCR antisense primer for subcloning EGF into DAV-1/EGF fusion construct.	
<400> 31 gaattetage geagtteeca ceaetteagg teteggtaet gacategete eeegatgtag ceaacaacae agttgeatge ataettgtee aatgette	60 98

<210> 32 <211> 27 <212> DNA <213> Artificial Sequence	
<220> <223> PCR sense primer for subcloning SCF into DAV-1/SCF fusion construct.	
<400> 32 gcggccgcaa gggatctgca ggaatcg	27
<210> 33 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> PCR antisense primer for subcloning SCF into DAV-1/SCF fusion construct.	
<400> 33 tctagagtgc aacagggggt aacata	26